

ES90

10/18

#5



OIPE

RAW SEQUENCE LISTING

DATE: 10/21/2002

PATENT APPLICATION: US/10/054,678

TIME: 17:05:10

Input Set : A:\2825.2012-004 Sequence Listing.txt
 Output Set: N:\CRF4\10212002\J054678.raw

ENTERED

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4 <110> APPLICANT: Sklar, Pamela
5   Lander, Eric S.
6   McInnis, Melvin G.
7   DePaulo, Jr., J. Raymond
8   Willour, Virginia
9   Potash, James
11 <120> TITLE OF INVENTION: ASSOCIATION OF DOPAMINE BETA-HYDROXYLASE
12   POLYMORPHISMS WITH BIPOLAR DISORDER
15 <130> FILE REFERENCE: 2825.2012-004
17 <140> CURRENT APPLICATION NUMBER: US 10/054,678
18 <141> CURRENT FILING DATE: 2002-01-22
20 <150> PRIOR APPLICATION NUMBER: US 09/852,967
21 <151> PRIOR FILING DATE: 2001-05-10
23 <150> PRIOR APPLICATION NUMBER: US 60/202,910
24 <151> PRIOR FILING DATE: 2000-05-10
26 <160> NUMBER OF SEQ ID NOS: 2
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2725
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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38 agagccccct cccctatcac atccccctgg acccggaggg gtccctggag ctctcatgg 180
39 atgtcagcta cacccaggag gccatccatt tccagctct ggtgcggagg ctcaaggctg 240
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42 acctggatcc ccagcaggac taccagctgc tgcaggtgca gaggacccca gaaggcctga 420
43 ccctgctttt caagggcccc ttggcacct gcgaccccaa ggattacctc attgaagacg 480
44 gcactgtcca cttggctcac gggatcctgg aggagccgtt ccggctcaact gaggccatca 540
45 acggctcggg cctgcagatg gggctgcaga ggggtcagct cctgaagccc aatatcccc 600
46 aaccggagtt gccctcagac gcgtgcacca tggaggtcca agctcccaat atccagatcc 660
47 ccagccagga gaccacgtac tggcttaca ttaaggagct tccaaagggc ttctctcgcc 720
48 accacattat caagtacgag cccatcgtca ccaaggggcaa tgaggccctt gtccaccaca 780
49 tggaaagtctt ccagtgcgc cccgagatgg acagcgtccc ccacttcagc gggccctgcg 840
50 actccaagat gaaaccgcac cgcctcaact actgcgcaca cgtgctggcc gcctggggcc 900
51 tgggtgccaa ggcattttac tacccagagg aagccggct tgccttcggg ggtccagggt 960
52 cctccagata tctccgcctg gaagttcaact accacaaccc actggtgata gaaggacgaa 1020
53 acgactcctc aggcatccgc ttgtactaca cagccaaagct gcggcgcttc aacgcgggaa 1080
54 tcatggagct gggactggtg tacacgcccag ttagtgcct tccaccacagg gagaccgcct 1140
55 tcatcctcac tggctactgc acggacaagt gcaccaggct gcactgcct ccctccggaa 1200
56 tccacatctt cgccttcag ctccacacac acctgactgg gagaaagggt gtcacagtgc 1260

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57 tggccggga cggccggag tgggagatcg tgaaccagga caatcaactac agccctcact 1320
 58 tccaggagat ccgcgttgc aagaaggctcg tgcgttcca tccgggagat gtgctcatca 1380
 59 cctcctgcac gtacaacacg gaagaccggg agctgccac agtgggggc ttccggatcc 1440
 60 tggaggagat gtgtcaac tacgtgcact actacccca gacgcagctg gagctctgca 1500
 61 agacggctgt ggacgcggc ttccgtcaga agtacttcca cctcatcaac aggttcaaca 1560
 62 acgaggatgt ctgcacctgc ctcaggcgt ccgtgtctca gcagttcacc tctgtccct 1620
 63 ggaactccctt caaccgcac gtactgaagg ccctgtacag cttcgcgcac atctccatgc 1680
 64 actgcaacaa gtcctcagcc gtccgttcc agggtgaatg gaacctgcag cccctgcaca 1740
 65 aggtcatctc cacactggaa gagccccccc cacagtgcac caccagccag ggcgaagcc 1800
 66 ctgctggccc caccgtgtc agcattgggt gggcaaagg ctgagggggg acctactct 1860
 67 cccctccctc catgctgtcc ctgtggctc acacccgcac tgtcactct actctgcgac 1920
 68 gatccccatg gaacagccct gcacgcggcag gatgaagggg ccagaccacg cccctgcctg 1980
 69 agaccacggc ccaatccagc ctctttcccc cagggtcccc tcgtggctg agagggtgtg 2040
 70 ggtccctgt tgacctaccc tggaccgagt ggaccacgac ctcgtccatt taaaccggc 2100
 71 tgactcagtg cagggacacgc ccccacatgt gtccagggtc cagccctccg ccagccctgt 2160
 72 tccgcctcac tgggtgtggc ctggcttctg ggacacggcac catgctggc cgggggtgtgg 2220
 73 aatcaccggg aacgcgcgcgc ccccccgcgc gctgtcccg gtgtgcagcg ggtgcgggtg 2280
 74 ccgcctaaac atttccctgc tgagtggctc gtgttcaca gtgggcggct tccctgcgac 2340
 75 ggaggcagga ccaggcattt agcttagttag agactcgct gggaaattgc tccattcctg 2400
 76 agtaaacaga tatttcgcgc cacctaaagg gaagccctga caacaactat cacaaaaga 2460
 77 cgaggcggca aagatccagc ggggcttctg ggcgcgggtt ccacgtgggg tggattatt 2520
 78 agcaccagct tgcttcgtc cccgtggggc cagcgtgaa cagaccgggg tggagtcaagg 2580
 79 gctgtgtttt ccgcgtgggtt ctgcccactta gggagtgtc cttggcggg ccatttcaca 2640
 80 ttccctgaccc tcactttct catctgtaaa accaggctga tgccgtgcgg gctaattgagc 2700
 81 caataaaagct cacacttggg ctggc 2725

83 <210> SEQ ID NO: 2

84 <211> LENGTH: 603

85 <212> TYPE: PRT

86 <213> ORGANISM: Homo sapiens

88 <400> SEQUENCE: 2

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91	Val	Ile	Leu	Val	Ala	Ala	Leu	Gln	Gly	Ser	Ala	Pro	Arg	Glu	Ser	Pro
92						20				25			30			
93	Leu	Pro	Tyr	His	Ile	Pro	Leu	Asp	Pro	Glu	Gly	Ser	Leu	Glu	Leu	Ser
94						35				40			45			
95	Trp	Asn	Val	Ser	Tyr	Thr	Gln	Glu	Ala	Ile	His	Phe	Gln	Leu	Leu	Val
96						50				55			60			
97	Arg	Arg	Leu	Lys	Ala	Gly	Val	Leu	Phe	Gly	Met	Ser	Asp	Arg	Gly	Glu
98	65						70				75			80		
99	Leu	Glu	Asn	Ala	Asp	Leu	Val	Val	Leu	Trp	Thr	Asp	Gly	Asp	Thr	Ala
100						85				90			95			
101	Tyr	Phe	Ala	Asp	Ala	Trp	Ser	Asp	Gln	Lys	Gly	Gln	Ile	His	Leu	Asp
102						100				105			110			
103	Pro	Gln	Gln	Asp	Tyr	Gln	Leu	Leu	Gln	Val	Gln	Arg	Thr	Pro	Glu	Gly
104						115				120			125			
105	Leu	Thr	Leu	Leu	Phe	Lys	Arg	Pro	Phe	Gly	Thr	Cys	Asp	Pro	Lys	Asp
106						130				135			140			
107	Tyr	Leu	Ile	Glu	Asp	Gly	Thr	Val	His	Leu	Val	Tyr	Gly	Ile	Leu	Glu

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108	145	150	155	160
109	Glu Pro Phe Arg Ser Leu Glu Ala Ile Asn Gly Ser Gly Leu Gln Met			
110	165	170	175	
111	Gly Leu Gln Arg Val Gln Leu Leu Lys Pro Asn Ile Pro Glu Pro Glu			
112	180	185	190	
113	Leu Pro Ser Asp Ala Cys Thr Met Glu Val Gln Ala Pro Asn Ile Gln			
114	195	200	205	
115	Ile Pro Ser Gln Glu Thr Thr Tyr Trp Cys Tyr Ile Lys Glu Leu Pro			
116	210	215	220	
117	Lys Gly Phe Ser Arg His His Ile Ile Lys Tyr Glu Pro Ile Val Thr			
118	225	230	235	240
119	Lys Gly Asn Glu Ala Leu Val His His Met Glu Val Phe Gln Cys Ala			
120	245	250	255	
121	Pro Glu Met Asp Ser Val Pro His Phe Ser Gly Pro Cys Asp Ser Lys			
122	260	265	270	
123	Met Lys Pro Asp Arg Leu Asn Tyr Cys Arg His Val Leu Ala Ala Trp			
124	275	280	285	
125	Ala Leu Gly Ala Lys Ala Phe Tyr Tyr Pro Glu Glu Ala Gly Leu Ala			
126	290	295	300	
127	Phe Gly Gly Pro Gly Ser Ser Arg Tyr Leu Arg Leu Glu Val His Tyr			
128	305	310	315	320
129	His Asn Pro Leu Val Ile Glu Gly Arg Asn Asp Ser Ser Gly Ile Arg			
130	325	330	335	
131	Leu Tyr Tyr Thr Ala Lys Leu Arg Arg Phe Asn Ala Gly Ile Met Glu			
132	340	345	350	
133	Leu Gly Leu Val Tyr Thr Pro Val Met Ala Ile Pro Pro Arg Glu Thr			
134	355	360	365	
135	Ala Phe Ile Leu Thr Gly Tyr Cys Thr Asp Lys Cys Thr Gln Leu Ala			
136	370	375	380	
137	Leu Pro Pro Ser Gly Ile His Ile Phe Ala Ser Gln Leu His Thr His			
138	385	390	395	400
139	Leu Thr Gly Arg Lys Val Val Thr Val Leu Val Arg Asp Gly Arg Glu			
140	405	410	415	
141	Trp Glu Ile Val Asn Gln Asp Asn His Tyr Ser Pro His Phe Gln Glu			
142	420	425	430	
143	Ile Arg Met Leu Lys Lys Val Val Ser Val His Pro Gly Asp Val Leu			
144	435	440	445	
145	Ile Thr Ser Cys Thr Tyr Asn Thr Glu Asp Arg Glu Leu Ala Thr Val			
146	450	455	460	
147	Gly Gly Phe Gly Ile Leu Glu Glu Met Cys Val Asn Tyr Val His Tyr			
148	465	470	475	480
149	Tyr Pro Gln Thr Gln Leu Glu Leu Cys Lys Thr Ala Val Asp Ala Gly			
150	485	490	495	
151	Phe Leu Gln Lys Tyr Phe His Leu Ile Asn Arg Phe Asn Asn Glu Asp			
152	500	505	510	
153	Val Cys Thr Cys Pro Gln Ala Ser Val Ser Gln Gln Phe Thr Ser Val			
154	515	520	525	
155	Pro Trp Asn Ser Phe Asn Arg Asp Val Leu Lys Ala Leu Tyr Ser Phe			
156	530	535	540	

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157 Ala Pro Ile Ser Met His Cys Asn Lys Ser Ser Ala Val Arg Phe Gln
158 545 550 555 560
159 Gly Glu Trp Asn Leu Gln Pro Leu Pro Lys Val Ile Ser Thr Leu Glu
160 565 570 575
161 Glu Pro Thr Pro Gln Cys Pro Thr Ser Gln Gly Arg Ser Pro Ala Gly
162 580 585 590
163 Pro Thr Val Val Ser Ile Gly Gly Lys Gly
164 595 600

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/054,678

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TIME: 17:05:11

Input Set : A:\2825.2012-004 Sequence Listing.txt

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